



SEQUENCE LISTING

<110> Bertin, John

<120> NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF

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<141> 2001-01-22

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<151> .2000-02-09

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cac ege cac agg ate gta ege tge ate tge eee age ege ete ace eee 329 His Arg His Arg Ile Val Arg Cys Ile Cys Pro Ser Arg Leu Thr Pro 30

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ctg cac agc ccc cgg ctc acc aac agc gcc atg cgg gcc ggg cac ttg 425 Leu His Ser Pro Arg Leu Thr Asn Ser Ala Met Arg Ala Gly His Leu 60

ctg gat ttg ctg aag act cga ggg aag aac ggg gcc atc gcc ttc ctg 473 Leu Asp Leu Leu Lys Thr Arg Gly Lys Asn Gly Ala Ile Ala Phe Leu 75





	agc Ser																521
	cag Gln																569
	aag Lys	Leu															617
	ctg Leu																665
	cag Gln 155																713
	cac His																761
	cac His																809
	ctg Leu																857
	tgc Cys																905
	cga Arg 235																953
	ctg Leu															1	001
	ctg Leu															1	049
	gag Glu															1	097
	cag Gln															1	145
gct	gcc	gag	agg	cag	cga	gag	cag	tac	tgg	gaa	gag	aag	gaa	cag	acc	1	193





Ala	Ala 315	Glu	Arg	Gln	Arg	Glu 320	Gln	Tyr	Trp	Glu	Glu 325	Lys	Glu	Gln	Thr	
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		aat Asn														1289
		gcg Ala														1337
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		gac Asp														1577
		agt Ser 460														1625
		ccc Pro														1673
		ttc Phe														1721
ccg Pro	gag Glu	gga Gly	gac Asp	ccg Pro 510	gga Gly	gcc Ala	ctg Leu	ccg Pro	gga Gly 515	gct Ala	aag Lys	gca Ala	ggc Gly	gac Asp 520	cca Pro	1769
		gat Asp														1817
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540	545	550

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	ggg Gly											20	09
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	tac Tyr 620											21	05
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	ctg Leu											22	49
	aac Asn											22	97
	aac Asn 700											23	45
	tgg Trp											23	93
	cac His						 _	_	_	_		24	41
	ctc Leu											24	89
	tct Ser											25	37

AI





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agc gag aa Ser Glu Ly			Phe Lys			2777
tac ttg ag Tyr Leu Se 86	r Gln Glu					2825
atc cag ga Ile Gln Gl 875						2873
gct gtg ga Ala Val Gl 890				s Āla Leu		2921
cag ctg ga Gln Leu As		Cys Thr			Phe P	2969
gtc atc ca Val Ile Hi			Met Ala			3017
ggc cta ca Gly Leu Gl 94	n Arg Leu					3065
agg cag ga Arg Gln Gl 955						3113
ctg gct cc Leu Ala Pr 970				/ Leu Leu		3161
cgc cag gc Arg Gln Al		Asp Glu			Thr G	3209







3931

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Lys Leu Arg Ser Leu Thr Phe Ser Leu Ala Glu Lys Asp Ile Leu Glu 275 280 Gln Ser Leu Asp Glu Ala Arg Gly Ser Arg Gln Glu Leu Val Glu Arg 295 Ile His Ser Leu Arg Glu Arg Ala Val Ala Ala Glu Arg Gln Arg Glu 310 315 Gln Tyr Trp Glu Glu Lys Glu Gln Thr Leu Leu Gln Phe Gln Lys Ser 325 330 Lys Met Ala Cys Gln Leu Tyr Arg Glu Lys Val Asn Ala Leu Gln Ala 345 Gln Val Cys Glu Leu Gln Lys Glu Arg Asp Gln Ala Tyr Ser Ala Arg 360 Asp Ser Ala Gln Arg Glu Ile Ser Gln Ser Leu Val Glu Lys Asp Ser 375 380 Leu Arg Arg Gln Val Phe Glu Leu Thr Asp Gln Val Cys Glu Leu Arg 390 395 Thr Gln Leu Arg Gln Leu Gln Ala Glu Pro Pro Gly Val Leu Lys Gln 405 410 Glu Ala Arg Thr Arg Glu Pro Cys Pro Arg Glu Lys Gln Arg Leu Val 420 425 Arg Met His Ala Ile Cys Pro Arg Asp Ser Asp Cys Ser Leu Val 440 445 Ser Ser Thr Glu Ser Gln Leu Leu Ser Asp Leu Ser Ala Thr Ser Ser 455 460 Arg Glu Leu Val Asp Ser Phe Arg Ser Ser Ser Pro Ala Pro Pro Ser 470 475 Gln Gln Ser Leu Tyr Lys Arg Val Ala Glu Asp Phe Gly Glu Glu Pro 485 490 Trp Ser Phe Ser Ser Cys Leu Glu Ile Pro Glu Gly Asp Pro Gly Ala 500 505 Leu Pro Gly Ala Lys Ala Gly Asp Pro His Leu Asp Tyr Glu Leu Leu 515 520 525 Asp Thr Ala Asp Leu Pro Gln Leu Glu Ser Ser Leu Gln Pro Val Ser 535 Pro Gly Arg Leu Asp Val Ser Glu Ser Gly Val Leu Met Arg Arg Arg 550 555 Pro Ala Arg Arg Ile Leu Ser Gln Val Thr Met Leu Ala Phe Gln Gly 570 Asp Ala Leu Leu Glu Gln Ile Ser Val Ile Gly Gly Asn Leu Thr Gly 585 580 Ile Phe Ile His Arg Val Thr Pro Gly Ser Ala Ala Asp Gln Met Ala 600 Leu Arg Pro Gly Thr Gln Ile Val Met Val Asp Tyr Glu Ala Ser Glu 615 620 Pro Leu Phe Lys Ala Val Leu Glu Asp Thr Thr Leu Glu Glu Ala Val 630 635 Gly Leu Leu Arg Arg Val Asp Gly Phe Cys Cys Leu Ser Val Lys Val 645 650 Asn Thr Asp Gly Tyr Lys Arg Leu Leu Gln Asp Leu Glu Ala Lys Val 665 Ala Thr Ser Gly Asp Ser Phe Tyr Ile Arg Val Asn Leu Ala Met Glu 680 Gly Arg Ala Lys Gly Glu Leu Gln Val His Cys Asn Glu Val Leu His 695 700 Val Thr Asp Thr Met Phe Gln Gly Cys Gly Cys Trp His Ala His Arg 710 715 Val Asn Ser Tyr Thr Met Lys Asp Thr Ala Ala His Gly Thr Ile Pro

AI

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Lys Leu Val Arg Ile Val Ser Met Asp Lys Ala Lys Ala Ser Pro Leu
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Ser Ser Thr Cys Phe Trp Ala Glu Ser Cys Leu Thr Leu Val Pro Tyr
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- -	-

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agc Ser	_	_		-			_	_	-	_	_	_		-	240
 aag Lys			_		_		_		_	_	_				288
gac Asp															336
aac Asn															384
agg Arg 130															432
ctg Leu															480
aac Asn															528
ctg Leu															576
cag Gln	_		_	-		_	_	_	_	-		_	_	-	624
ttc Phe 210															672
cac His															720
cgc Arg															768
gcc Ala															816

A

ctg Leu	agg Arg	aca Thr 275	gcc Ala	agc Ser	gac Asp	cag Gln	gag Glu 280	tcc Ser	ggg Gly	gat Asp	gag Glu	gag Glu 285	ctg Leu	aac Asn	cgc Arg	864
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							cac His									1008
							gcc Ala									1056
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A

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					gag Glu												1728
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					ggc Gly										gcc Ala	,	2016
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M

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955

960

950

Al

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Al

465 470 475 Asp Ser Asp Cys Ser Leu Val Ser Ser Thr Glu Ser Gln Leu Leu Ser 485 490 Asp Leu Ser Ala Thr Ser Ser Arg Glu Leu Val Asp Ser Phe Arg Ser 500 505 Ser Ser Pro Ala Pro Pro Ser Gln Gln Ser Leu Tyr Lys Arg Val Ala 520 Glu Asp Phe Gly Glu Glu Pro Trp Ser Phe Ser Ser Cys Leu Glu Ile 535 540 Pro Glu Gly Asp Pro Gly Ala Leu Pro Gly Ala Lys Ala Gly Asp Pro 550 555 His Leu Asp Tyr Glu Leu Leu Asp Thr Ala Asp Leu Pro Gln Leu Glu 565 570 Ser Ser Leu Gln Pro Val Ser Pro Gly Arg Leu Asp Val Ser Glu Ser 585 Ala Gln Ala Gly Arg Leu Pro Ala Cys Ser Gly Val Leu Met Arg Arg 600 Arg Pro Ala Arg Arg Ile Leu Ser Gln Val Thr Met Leu Ala Phe Gln 615 620 Gly Asp Ala Leu Leu Glu Gln Ile Ser Val Ile Gly Gly Asn Leu Thr 630 635 Gly Ile Phe Ile His Arg Val Thr Pro Gly Ser Ala Ala Asp Gln Met 645 650 Ala Leu Arg Pro Gly Thr Gln Ile Val Met Val Asp Tyr Glu Ala Ser 660 665 Glu Pro Leu Phe Lys Ala Val Leu Glu Asp Thr Thr Leu Glu Glu Ala 675 680 Val Gly Leu Leu Arg Arg Val Asp Gly Phe Cys Cys Leu Ser Val Lys 695 700 Val Asn Thr Asp Gly Tyr Lys Arg Leu Leu Gln Asp Leu Glu Ala Lys 710 Val Ala Thr Ser Gly Asp Ser Phe Tyr Ile Arg Val Asn Leu Ala Met 725 730 Glu Gly Arg Ala Lys Gly Glu Leu Gln Val His Cys Asn Glu Val Leu 740 745 His Val Thr Asp Thr Met Phe Gln Gly Cys Gly Cys Trp His Ala His 760 Arg Val Asn Ser Tyr Thr Met Lys Asp Thr Ala Ala His Gly Thr Ile 775 780 Pro Asn Tyr Ser Arg Ala Gln Gln Leu Ile Ala Leu Ile Gln Asp 790 795 Met Thr Gln Gln Cys Thr Val Thr Arg Lys Pro Ser Ser Gly Gly Pro 810 Gln Lys Leu Val Arg Ile Val Ser Met Asp Lys Ala Lys Ala Ser Pro 820 825 Leu Arg Leu Ser Phe Asp Arg Gly Gln Leu Asp Pro Ser Arg Met Glu 840 845 Gly Ser Ser Thr Cys Phe Trp Ala Glu Ser Cys Leu Thr Leu Val Pro 855 Tyr Thr Leu Val Arg Pro His Arg Pro Ala Arg Pro Arg Pro Val Leu 870 875 Leu Val Pro Arg Ala Val Gly Lys Ile Leu Ser Glu Lys Leu Cys Leu 885 890 Leu Gln Gly Phe Lys Lys Cys Leu Ala Glu Tyr Leu Ser Gln Glu Glu 905 Tyr Glu Ala Trp Ser Gln Arg Gly Asp Ile Ile Gln Glu Gly Glu Val 915 920

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Ser Gly Gly Arg Cys Trp Val Thr Arg His Ala Val Glu Ser Leu Met 935 940 Glu Lys Asn Thr His Ala Leu Leu Asp Val Gln Leu Asp Ser Val Cys 950 955 Thr Leu His Arg Met Asp Ile Phe Pro Ile Val Ile His Val Ser Val 965 970 Asn Glu Lys Met Ala Lys Lys Leu Lys Lys Gly Leu Gln Arg Leu Gly 985 Thr Ser Glu Glu Gln Leu Leu Glu Ala Ala Arg Gln Glu Glu Gly Asp 1000 Leu Asp Arg Ala Pro Cys Leu Tyr Ser Ser Leu Ala Pro Asp Gly Trp 1015 1020 Ser Asp Leu Asp Gly Leu Leu Ser Cys Val Arg Gln Ala Ile Ala Asp 1030 1035 Glu Gln Lys Lys Val Gln Arg Arg Arg His Pro Arg Ile Asn Pro Ser 1045 1050 Gln Arg Thr Gly Ile Ala Thr Gln Gln Arg Gln Cys His Arg Arg Ile 1060 1065 1070 Asn Pro Arg Gln Arg Met Gly Ile Ala Thr Gln Gln Arg Gln Cys His 1075 1080 Arg Arg Ile Asn Pro Ser Gln Arg Thr Gly Ile Thr Thr Gln Gln Cys 1095 1100 Gln Cys His Arg Arg Ile Asn Pro Ser Gln Arg Thr Gly Ile Ala Met 1110 1115 Pro Ser Ser Asp Thr Leu Lys Lys Asp Lys Leu Leu Pro Arg Asn 1125 1130 Thr Thr <210> 6 <211> 90 <212> PRT <213> Artificial Sequence <220> <223> consensus sequence <400> 6 Ala Glu Asp Asp Arg Arg Leu Leu Arg Lys Asn Arg Leu Glu Leu Leu 10 Gly Glu Leu Thr Leu Ser Gly Leu Leu Asp His Leu Leu Glu Lys Asn 25 Val Leu Thr Glu Glu Glu Glu Lys Ile Lys Ala Lys Asn Thr Thr 40 Arg Arg Asp Lys Ala Arg Glu Leu Ile Asp Ser Val Gln Lys Lys Gly 55 Asn Gln Ala Phe Gly Ile Phe Leu Gln Ala Leu Arg Glu Thr Asp Gly 70 Glu Leu Leu Ala Asp Leu Leu Leu Asp Glu 85 <210> 7 <211> 83 <212> PRT <213> Artificial Sequence <220>

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Gly Ser Leu Ser Leu Lys Glu Leu Gln Gln Leu Glu Gln Gln Leu Glu
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Lys Gly Leu Lys His Ile Arg Ser Arg Lys Asn Gln Leu Leu Leu Asp
Gln Ile Glu Glu Leu Gln Lys Lys Glu Arg Glu Leu Gln Glu Glu Asn
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Lys Ala Leu Arg Lys Lys Ile Glu Glu
            100
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